



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/507,446

Source:

PT/10

Date Processed by STIC:

9/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202



PCT

## RAW SEQUENCE LISTING

DATE: 09/23/2004

PATENT APPLICATION: US/10/507,446

TIME: 11:50:43

Input Set : A:\Sequence Listing PCT JP0302946.txt

Output Set: N:\CRF4\09232004\J507446.raw

3 <110> APPLICANT: GOTO, Hidetsugu  
 4 NAKANO, Shigeru  
 6 <120> TITLE OF INVENTION: Structural gene responsible for acetic acid resistance in  
 acetic  
 7 acid bacteria, acetic acid bacteria transformed with said gene,  
 8 and acetic acid fermentation using said transformations  
 10 <130> FILE REFERENCE: 4439-4024  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/507,446  
 C--> 13 <141> CURRENT FILING DATE: 2004-09-13  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02946  
 16 <151> PRIOR FILING DATE: 2003-03-12  
 18 <160> NUMBER OF SEQ ID NOS: 10  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 2016  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Gluconacetobacter entanii  
 27 <400> SEQUENCE: 1

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30	aattttgtca tggaaatcga ggacacgctc gacgtttccg tgccgcttga ccggctggct	120
32	gatatccgca ccattgatga tctggctgcc tgtatcgtct ctctcaagca ggcatcctga	180
34	tacaccatgt cgattttctc gaaatatgaa ggccttgctg ccgccctgtc ggccggtaacg	240
36	gccgatggtg ggcgcaaccc gttcaacgct gtgatcgaaa agcccatctc ctccacggctc	300
38	gggctgatcg aaggcgcgca gacgcttctg ttccggacca acaactatct tgggctgagc	360
40	cagtccccgg ccgcatcgca agcggcggtg gaagccgcca gggcttatgg tgtcggcagc	420
42	accggatcgc gcatcgccaa tggcagcgag ggtctgcacc gccagttgga agagcggctg	480
44	tgcaccttct tccgtcgtcg gcactgcatg gtgttttcca ccggttacca ggccaatctg	540
46	ggcacgattt ccgcactggc gggcaaggac gattatctgc tgcttgatgc ggacagccat	600
48	gccagcatct atgatggcag ccgccttggc catcgcgagg tcatccgctt ccgtcacaac	660
50	gacgccgatg acctgcataa acgcctgcgc cgccttgatg gtacgcccgg agcgaaactg	720
52	gtcgtggtcg aaggcatcta ttccatgatg ggcgacgtcg ttcccatggc ggaattcgcg	780
54	gccgtcaagc gggaaaccgg tgcattgctg ctggcggtatg aagcacattc cgttggtgta	840
56	atgggcgaac atggccgtgg cgtggcgga tccgacggcg tggagatga tgtcgatttt	900
58	gtcgtcggca ctttttccaa aagccttggc acggttggtg gctactgtgt ttccaaccat	960
60	gccgggctgg acctgatccg gctgtgttcg cgtccgtaca tgttcaccgc atccctgccc	1020
62	ccggaagtca tcgccgcgac catggccgcg ctgactgaac tggaaaaccg gccggaactg	1080
64	cgcgtgcggt tgatggacaa tgcacgcagg cttcatgacg ggctgcaggc ggccggcctg	1140
66	cgcaccggcc cgcaggccag tcctgtcgtg tccgtcattc tggatgatgt ggccggttgcc	1200
68	gtggcggttct ggaaccggct gctggacctt ggggtttacg tcaacctcag cctgccgcct	1260
70	gcaacgcccg accagcatcc cctgctgcgg acctccgtca tggcgaccca tacgccggag	1320
72	cagatagacc gggccgtgga aatcttcgcc gttgtagcgg gcgagatggg tatcaaccgc	1380
74	gccgcctgaa aaaacctgcc tgccgtaatt tccacagcag atacggcagg cagaccagcg	1440
76	gatgccgttc cgaaaacggc cccagcggca gttcaatgcc ggaatgccgc ctgatcttcc	1500
78	atgcgatata gcgcgcgcca ctttcaaacg tgaaggcccc cttgaacagg cggctgacat	1560

Does Not Comply  
 Corrected Diskette Needed

pp. 5-6

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/507,446

DATE: 09/23/2004

TIME: 11:50:43

Input Set : A:\Sequence Listing PCT JP0302946.txt

Output Set: N:\CRF4\09232004\J507446.raw

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80 tcagcacgcg cccagccga ccacgcagcc accagccttc gtacatcttc cggcgagtt 1620
82 caggtgtcag ctggggggtt agttgatcgc cctcagaccg gaacggcagg ccatcggcgc 1680
84 gccatacatc cggcagcagg cgctgtacc gtgttctctg cccctgtagc aggctacgcg 1740
86 gcctgcggcc gttctccaca cgcagttccg caccgtaagt atgggcgaac agggccagcc 1800
88 agtagtcatc ggccgtgccc tgtgccggac ccagggcggc agcccagcgc cccgcctgcc 1860
90 ccaccgcgcg gataatgcag gccaggatgg catcggccgc gtccggttcc ctgaccata 1920
92 caagccgcac aggctggcag aagcgtgccc agaccgtggt atccaacgtg gcgcgtcccg 1980
94 tcatgcggcg gaactgcgct atggacagga tggcca 2016
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98 <211> LENGTH: 400
99 <212> TYPE: PRT
100 <213> ORGANISM: Gluconacetobacter entanii
102 <400> SEQUENCE: 2
104 Met Ser Ile Phe Ser Lys Tyr Glu Gly Leu Ala Ser Ala Leu Ser Ala
105 1 5 10 15
108 Val Thr Ala Asp Gly Gly Arg Asn Pro Phe Asn Val Val Ile Glu Lys
109 20 25 30
112 Pro Ile Ser Ser Thr Val Gly Leu Ile Glu Gly Arg Glu Thr Leu Leu
113 35 40 45
116 Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Pro Ala Ala Ile
117 50 55 60
120 Glu Ala Ala Val Glu Ala Ala Arg Ala Tyr Gly Val Gly Thr Thr Gly
121 65 70 75 80
124 Ser Arg Ile Ala Asn Gly Thr Gln Gly Leu His Arg Gln Leu Glu Glu
125 85 90 95
128 Arg Leu Cys Thr Phe Phe Arg Arg Arg His Cys Met Val Phe Ser Thr
129 100 105 110
132 Gly Tyr Gln Ala Asn Leu Gly Thr Ile Ser Ala Leu Ala Gly Lys Asp
133 115 120 125
136 Asp Tyr Leu Leu Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp Gly
137 130 135 140
140 Ser Arg Leu Gly His Ala Gln Val Ile Arg Phe Arg His Asn Asp Ala
141 145 150 155 160
144 Asp Asp Leu His Lys Arg Leu Arg Arg Leu Asp Gly Thr Pro Gly Ala
145 165 170 175
148 Lys Leu Val Val Val Glu Gly Ile Tyr Ser Met Met Gly Asp Val Val
149 180 185 190
152 Pro Met Ala Glu Phe Ala Ala Val Lys Arg Glu Thr Gly Ala Trp Leu
153 195 200 205
156 Leu Ala Asp Glu Ala His Ser Val Gly Val Met Gly Glu His Gly Arg
157 210 215 220
160 Gly Val Ala Glu Ser Asp Gly Val Glu Asp Asp Val Asp Phe Val Val
161 225 230 235 240
164 Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val Ser
165 245 250 255
168 Asn His Ala Gly Leu Asp Leu Ile Arg Leu Cys Ser Arg Pro Tyr Met
169 260 265 270
172 Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Met Ala Ala
173 275 280 285

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176 Leu Thr Glu Leu Glu Asn Arg Pro Glu Leu Arg Val Arg Leu Met Asp
177      290                      295                      300
180 Asn Ala Arg Arg Leu His Asp Gly Leu Gln Ala Ala Gly Leu Arg Thr
181 305                      310                      315                      320
184 Gly Pro Gln Ala Ser Pro Val Val Ser Val Ile Leu Asp Asp Val Ala
185                      325                      330                      335
188 Val Ala Val Ala Phe Trp Asn Arg Leu Leu Asp Leu Gly Val Tyr Val
189                      340                      345                      350
192 Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Gln His Pro Leu Leu Arg
193                      355                      360                      365
196 Thr Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Asp Arg Ala Val
197      370                      375                      380
200 Glu Ile Phe Ala Val Val Ala Gly Glu Met Gly Ile Asn Arg Ala Ala
201 385                      390                      395                      400
204 <210> SEQ ID NO: 3
205 <211> LENGTH: 1360
206 <212> TYPE: DNA
207 <213> ORGANISM: Acetobacter aceti
209 <400> SEQUENCE: 3
210 gaagacagct tggatgtatc tatcccgcgc gacaaactgg ctgatatccg aacgattaat      60
212 gaccttgccg cttgcattgt tgctctgaaa aacaaagggg gaggcgtgga tgacatcact      120
214 attttccaaa tttgaaggta cggcaggcgc gctgggttcc gttgtggccg taggcggtcg      180
216 caaccctttt gctgttggtt ttgaaaaacc tgtctcttca actgttggaa ttattgaagg      240
218 tcgggaaacg cttctttttg gcaccaataa ctatttgggg cttagtcaat ccaaaaatgc      300
220 cattcaagca gccacgcagg ctgccgcggc atgtggcgta ggcacaacgg gctcacgcat      360
222 tgcaaatggc acacaatccc tgcaccgaca gcttgaaaaa gatattgccg cgtttttttg      420
224 tcggcgatgat gccatggttt tttccacggg gtatcaggca aacctcggca ttatttccac      480
226 gctggcaggt aaggatgacc acctgtttct ggatgctgat agccacgcca gtatctatga      540
228 tggcagccgc ctgagtgcag cagaagttat tcgcttccgc cataatgatc cagacaacct      600
230 ttataaacgc cttaaacgca tggatggcac gccaggcgcc aaattgattg tggttgaagg      660
232 catttattcc atgacgggta atgttgcccc gattgcagaa tttgttgctg ttaaaaaaga      720
234 aacaggcgct tacctgctgg tagatgaagc ccattctttt ggcgtgttgg gtcaaaatgg      780
236 gcgtgggtgcc gctgaggctg atggcggtga agctgatgtg gactttgttg tcggcacatt      840
238 ttccaaaagc ttgggcacag ttggcggtta ctgcgtatct gaccatcctg agctggagtt      900
240 tgtgcgctta aactgccggc cctatatgtt tacggcatcg ctaccgccgg aagttattgc      960
242 tgccacaacg gctgccttga aagatatgca ggcacatcct gaattgcgta agcagcttat      1020
244 ggcaaacgcg cagcaactac atgcaggttt tgtagatatt gggctaaatg ccagcaaaca      1080
246 cgcaacccca gttattgccg ttacattgga aacagctgaa gaagctattc ccatgtggaa      1140
248 caggcttttg gaacttggtg tttatgtaaa tctcagcctt cctccggcta caccagattc      1200
250 gcggccggtt ctccgttggt ccgtaatggc caccatacgc ccgaacaaa ttgcgcaggc      1260
252 tattgccata ttcaggcagg ctgcggcaga agtaggcgta accatcacac cctccgctgc      1320
254 ttaaaaaaaaa gctatttgcg cttgaatgcc ccttgctgcc      1360
257 <210> SEQ ID NO: 4
258 <211> LENGTH: 404
259 <212> TYPE: PRT
260 <213> ORGANISM: Acetobacter aceti
262 <400> SEQUENCE: 4
264 Met Thr Ser Leu Phe Ser Lys Phe Glu Gly Thr Ala Gly Ala Leu Gly
265 1                      5                      10                      15

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Input Set : A:\Sequence Listing PCT JP0302946.txt

Output Set: N:\CRF4\09232004\J507446.raw

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268 Ser Val Val Ala Val Gly Gly Arg Asn Pro Phe Ala Val Val Ile Glu
269          20          25          30
272 Lys Pro Val Ser Ser Thr Val Gly Ile Ile Glu Gly Arg Glu Thr Leu
273          35          40          45
276 Leu Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Lys Asn Ala
277          50          55          60
280 Ile Gln Ala Ala Gln Gln Ala Ala Ala Cys Gly Val Gly Thr Thr
281 65          70          75          80
284 Gly Ser Arg Ile Ala Asn Gly Thr Gln Ser Leu His Arg Gln Leu Glu
285          85          90          95
288 Lys Asp Ile Ala Ala Phe Phe Gly Arg Arg Asp Ala Met Val Phe Ser
289          100          105          110
292 Thr Gly Tyr Gln Ala Asn Leu Gly Ile Ile Ser Thr Leu Ala Gly Lys
293          115          120          125
296 Asp Asp His Leu Phe Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp
297          130          135          140
300 Gly Ser Arg Leu Ser Ala Ala Glu Val Ile Arg Phe Arg His Asn Asp
301 145          150          155          160
304 Pro Asp Asn Leu Tyr Lys Arg Leu Lys Arg Met Asp Gly Thr Pro Gly
305          165          170          175
308 Ala Lys Leu Ile Val Val Glu Gly Ile Tyr Ser Met Thr Gly Asn Val
309          180          185          190
312 Ala Pro Ile Ala Glu Phe Val Ala Val Lys Lys Glu Thr Gly Ala Tyr
313          195          200          205
316 Leu Leu Val Asp Glu Ala His Ser Phe Gly Val Leu Gly Gln Asn Gly
317          210          215          220
320 Arg Gly Ala Ala Glu Ala Asp Gly Val Glu Ala Asp Val Asp Phe Val
321 225          230          235          240
324 Val Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val
325          245          250          255
328 Ser Asp His Pro Glu Leu Glu Phe Val Arg Leu Asn Cys Arg Pro Tyr
329          260          265          270
332 Met Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Thr Ala
333          275          280          285
336 Ala Leu Lys Asp Met Gln Ala His Pro Glu Leu Arg Lys Gln Leu Met
337          290          295          300
340 Ala Asn Ala Gln Gln Leu His Ala Gly Phe Val Asp Ile Gly Leu Asn
341 305          310          315          320
344 Ala Ser Lys His Ala Thr Pro Val Ile Ala Val Thr Leu Glu Thr Ala
345          325          330          335
348 Glu Glu Ala Ile Pro Met Trp Asn Arg Leu Leu Glu Leu Gly Val Tyr
349          340          345          350
352 Val Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Ser Arg Pro Leu Leu
353          355          360          365
356 Arg Cys Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Ala Gln Ala
357          370          375          380
360 Ile Ala Ile Phe Arg Gln Ala Ala Ala Glu Val Gly Val Thr Ile Thr
361 385          390          395          400
364 Pro Ser Ala Ala

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PATENT APPLICATION: US/10/507,446

DATE: 09/23/2004

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Input Set : A:\Sequence Listing PCT JP0302946.txt

Output Set: N:\CRF4\09232004\J507446.raw

368 <210> SEQ ID NO: 5  
 369 <211> LENGTH: 30  
 370 <212> TYPE: DNA  
 C--> 371 <213> ORGANISM: Artificial Sequence  
 W--> 373 <220> FEATURE:  
 W--> 373 <223> OTHER INFORMATION:  
 W--> 373 <400> 5  
 374 ctggctgcct gtatcgtctc tctcaagcag 30  
 377 <210> SEQ ID NO: 6  
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 379 <212> TYPE: DNA  
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 383 acggctgcag ctggtctgcc tgccgtatct 30  
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 388 <212> TYPE: DNA  
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 396 <211> LENGTH: 29  
 397 <212> TYPE: DNA  
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 404 <210> SEQ ID NO: 9  
 405 <211> LENGTH: 30  
 406 <212> TYPE: DNA  
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 W--> 409 <223> OTHER INFORMATION:  
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 410 gccagcgtgg aaataatgcc gaggtttgcc 30  
 413 <210> SEQ ID NO: 10  
 414 <211> LENGTH: 29  
 415 <212> TYPE: DNA  
 C--> 416 <213> ORGANISM: Artificial Sequence  
 W--> 418 <220> FEATURE:  
 W--> 418 <223> OTHER INFORMATION:  
 W--> 418 <400> 10  
 419 cagccttccct ccggtacac cagattcgc 29

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/507,446

DATE: 09/23/2004  
TIME: 11:50:44

Input Set : A:\Sequence Listing PCT JP0302946.txt  
Output Set: N:\CRF4\09232004\J507446.raw

*error explanation*

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:5,6,7,8,9,10

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/507,446

DATE: 09/23/2004

TIME: 11:50:44

Input Set : A:\Sequence Listing PCT JP0302946.txt

Output Set: N:\CRF4\09232004\J507446.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:371 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:373 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>  
ORGANISM:Artificial Sequence  
L:373 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>  
ORGANISM:Artificial Sequence  
L:373 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:373  
L:380 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:382 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>  
ORGANISM:Artificial Sequence  
L:382 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>  
ORGANISM:Artificial Sequence  
L:382 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:382  
L:389 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:391 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>  
ORGANISM:Artificial Sequence  
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L:391 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:391  
L:398 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:400 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>  
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L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:400  
L:407 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:409 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>  
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L:409 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>  
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L:409 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:409  
L:416 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:418 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>  
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